

Fig. 1.

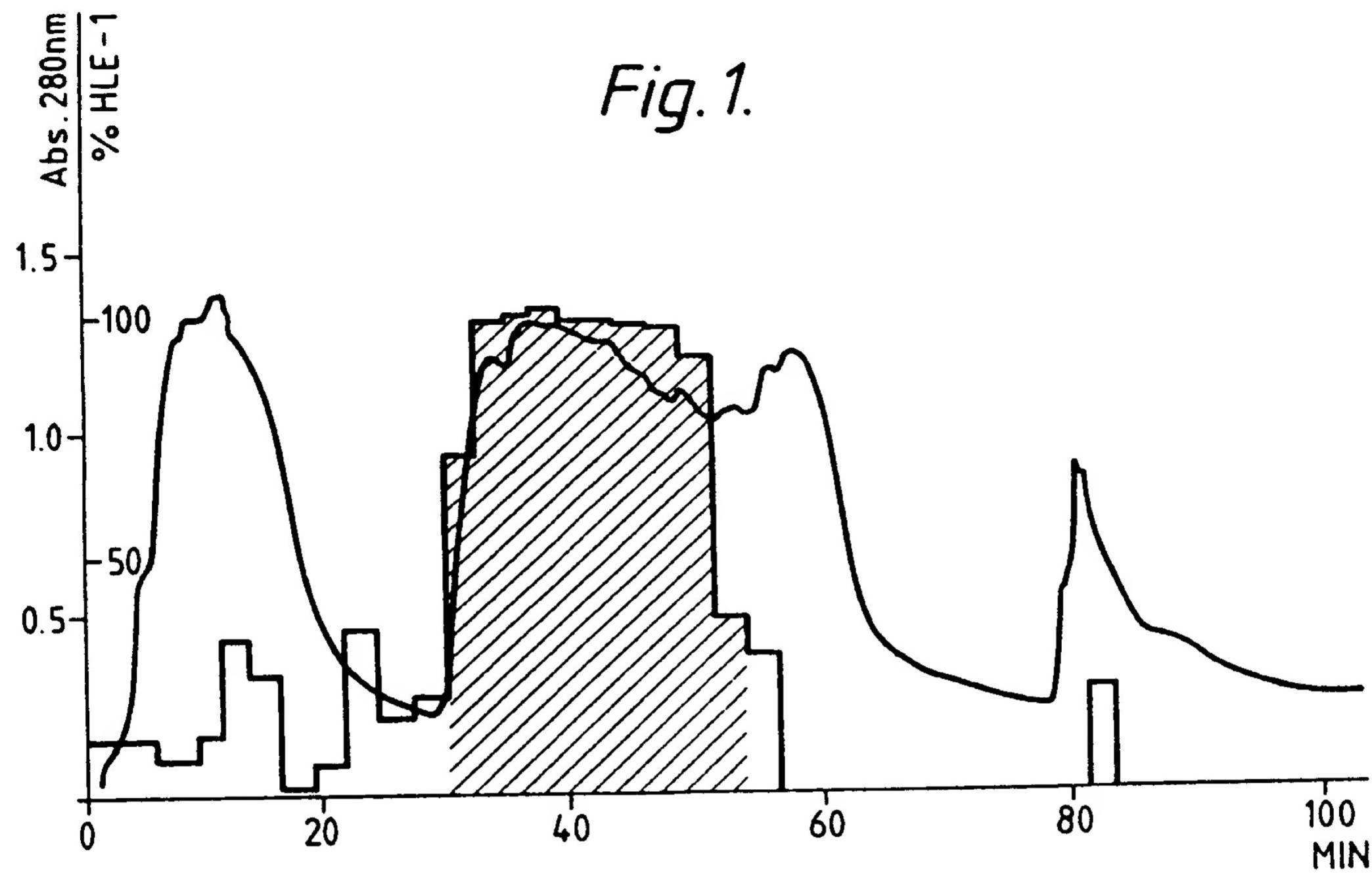


Fig. 2.

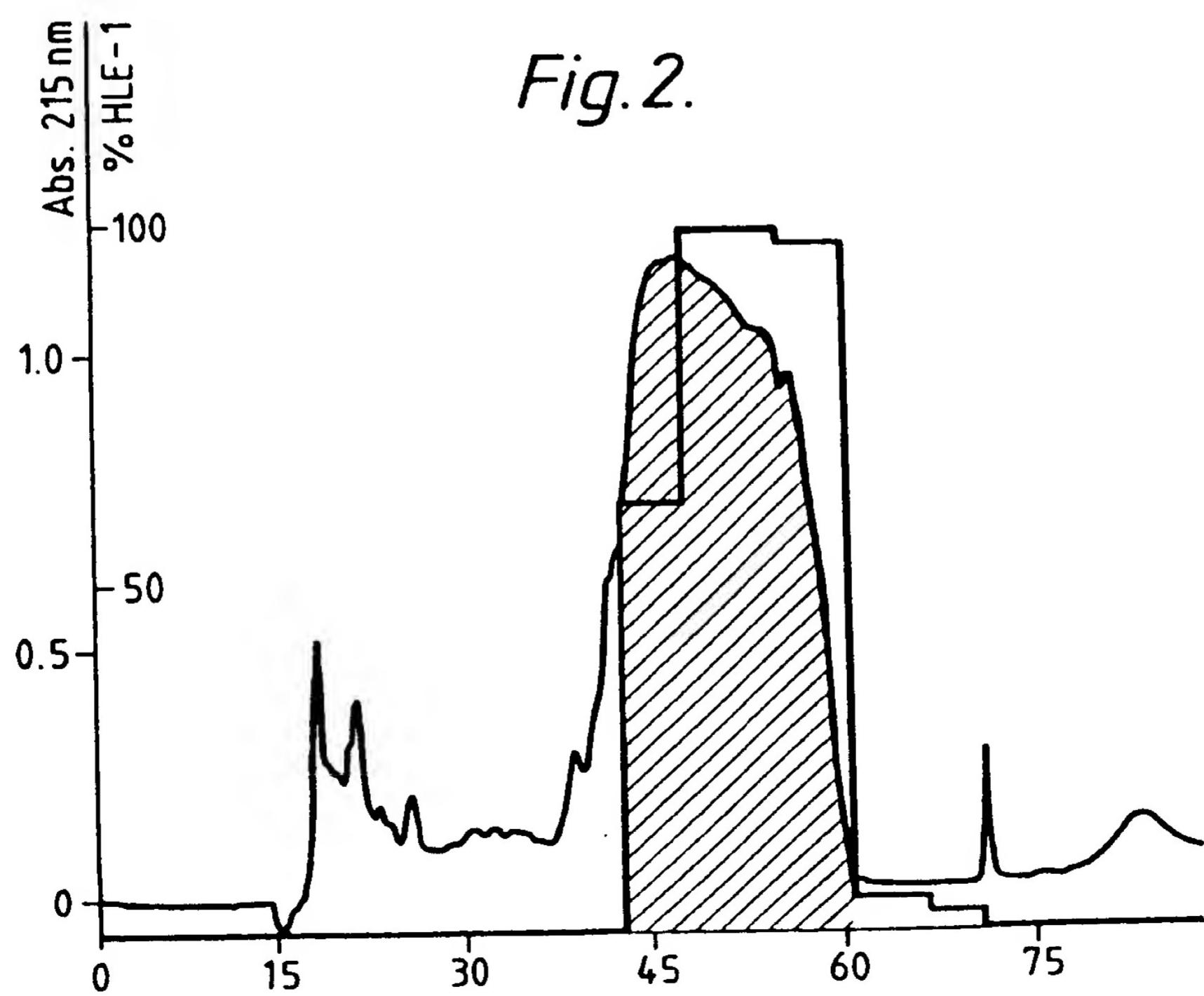


Fig. 3. HPLC chromatogram showing Abs. 220nm / % HLE-1 vs ml.

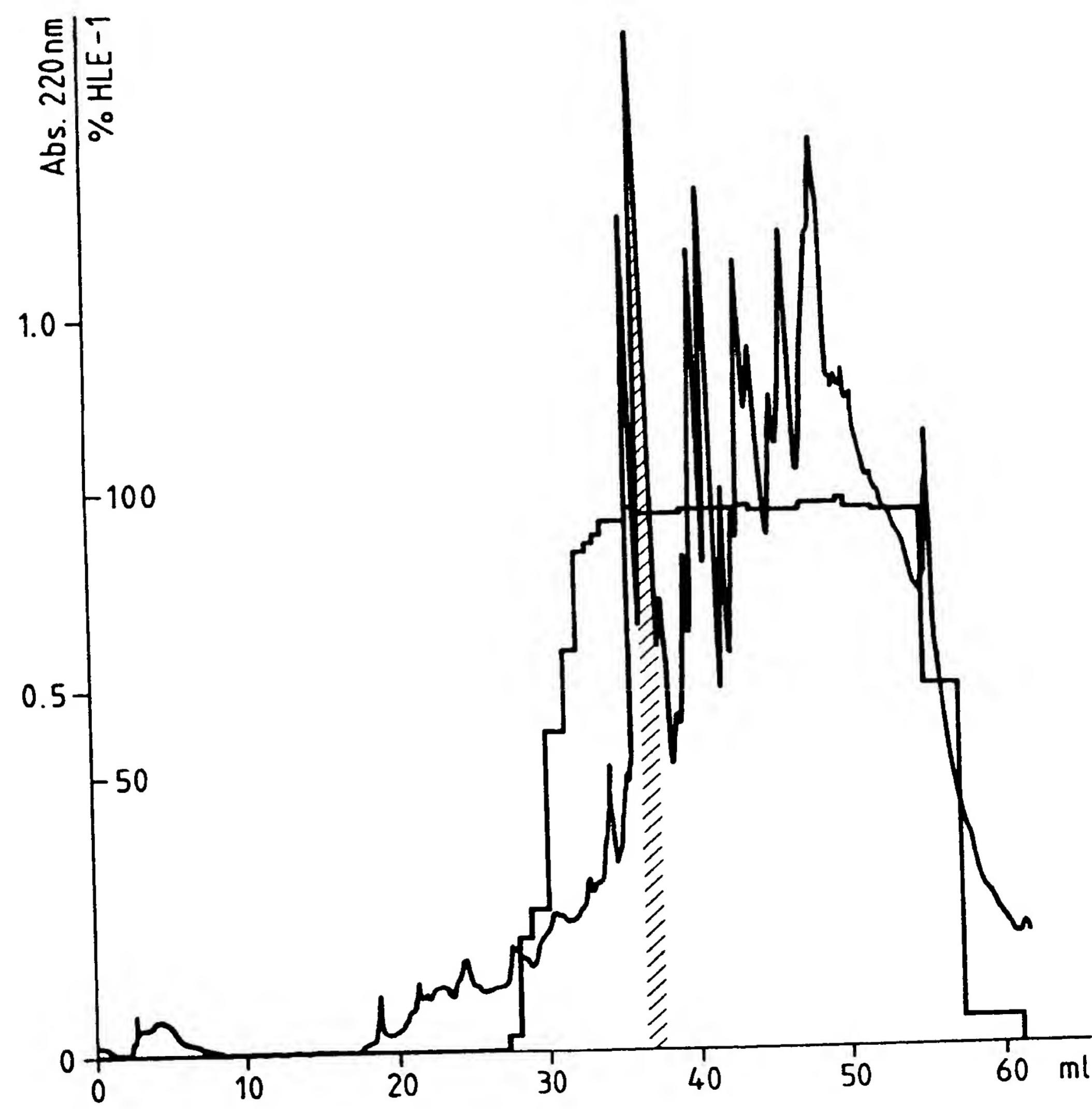


Fig. 3.

Fig. 4.

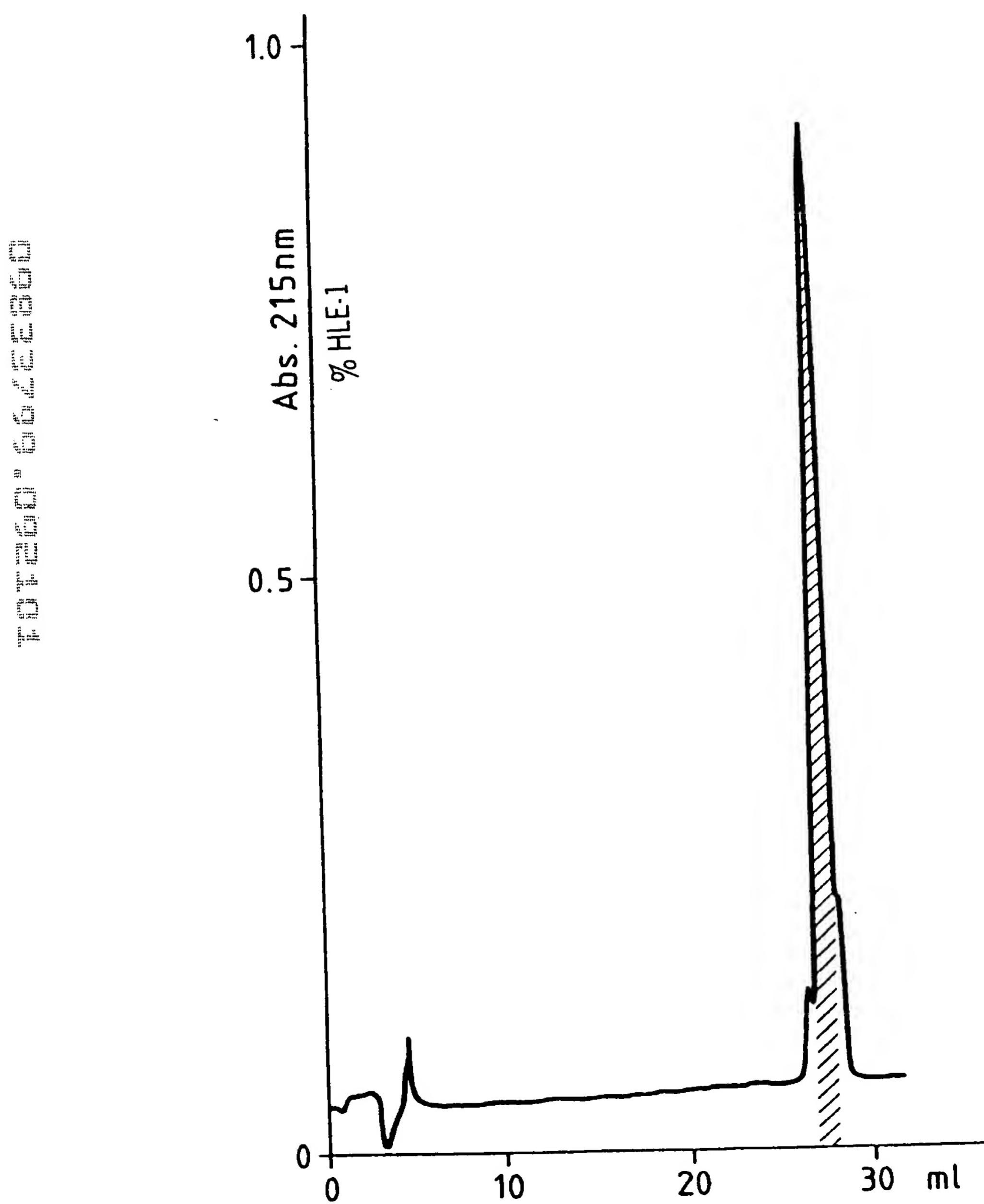


Fig. 5.

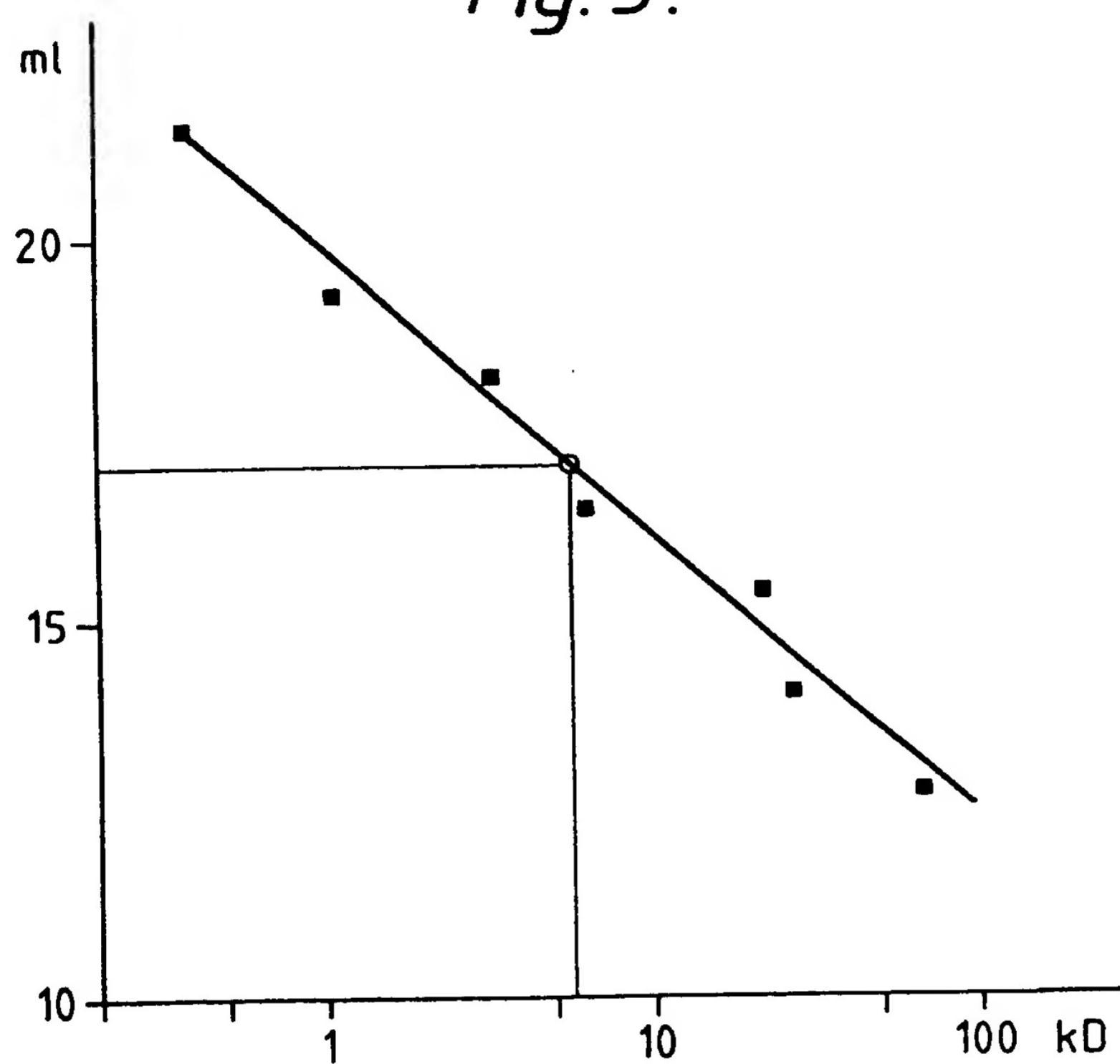


Fig. 7.

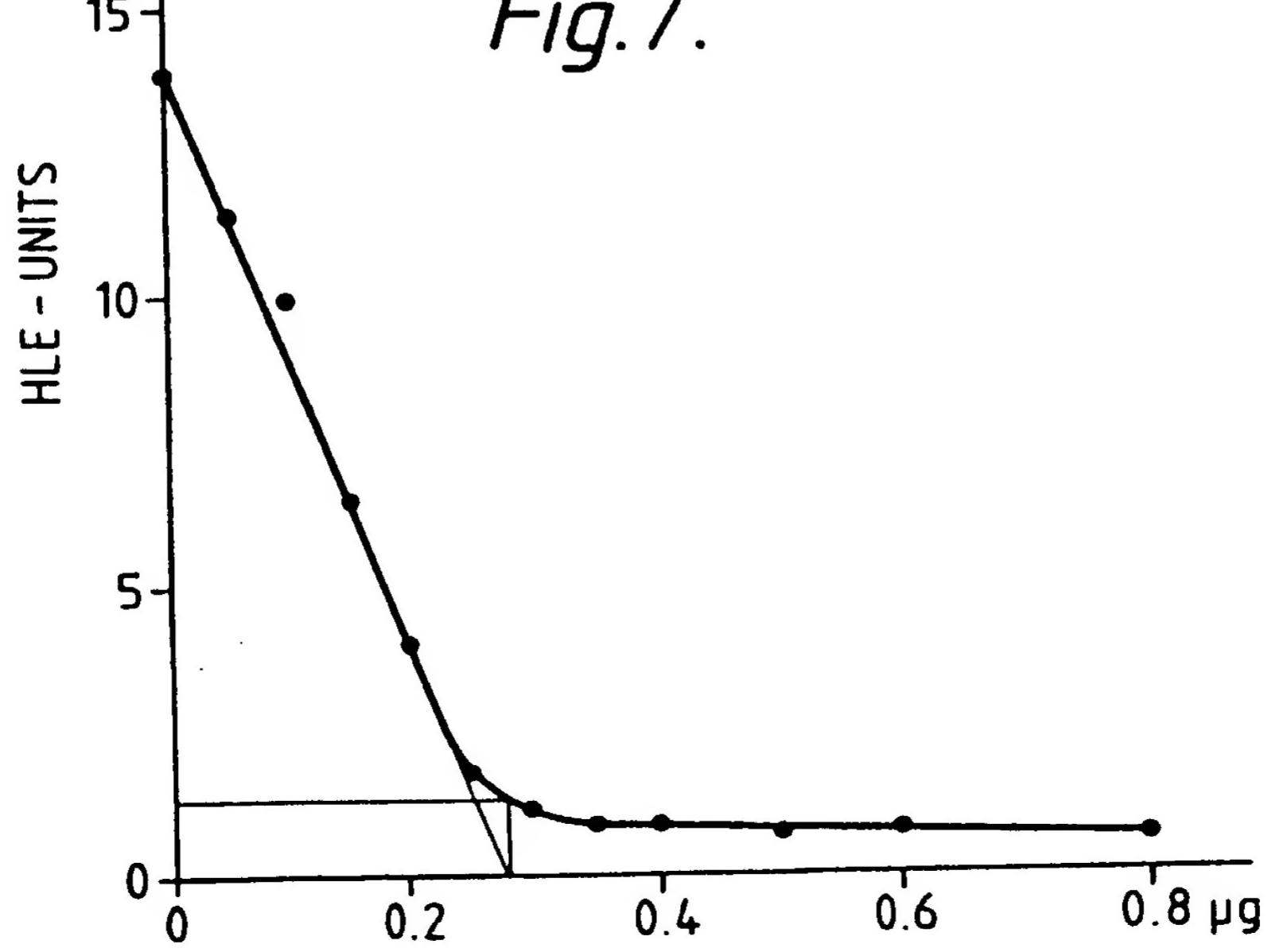


Fig. 6.

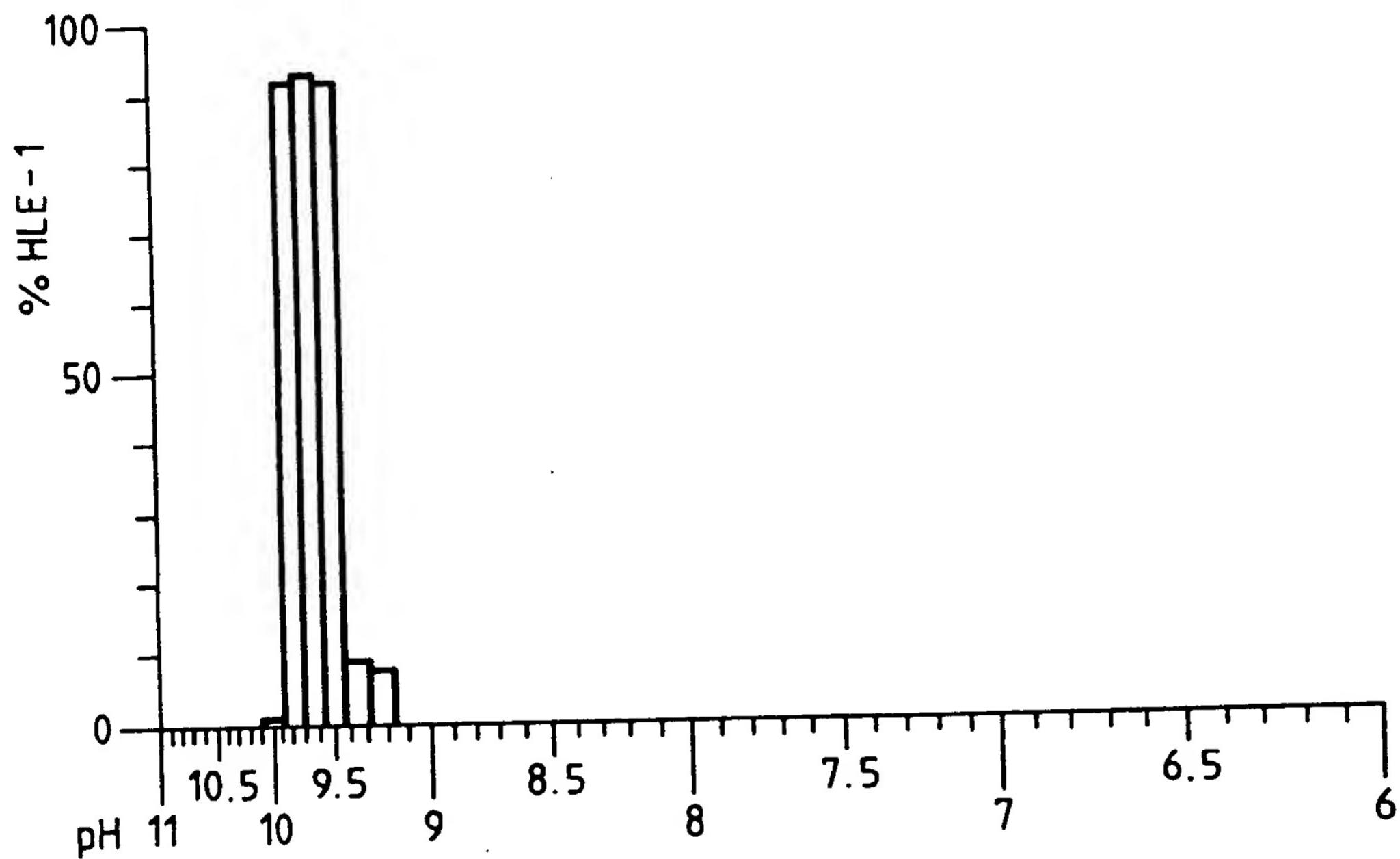
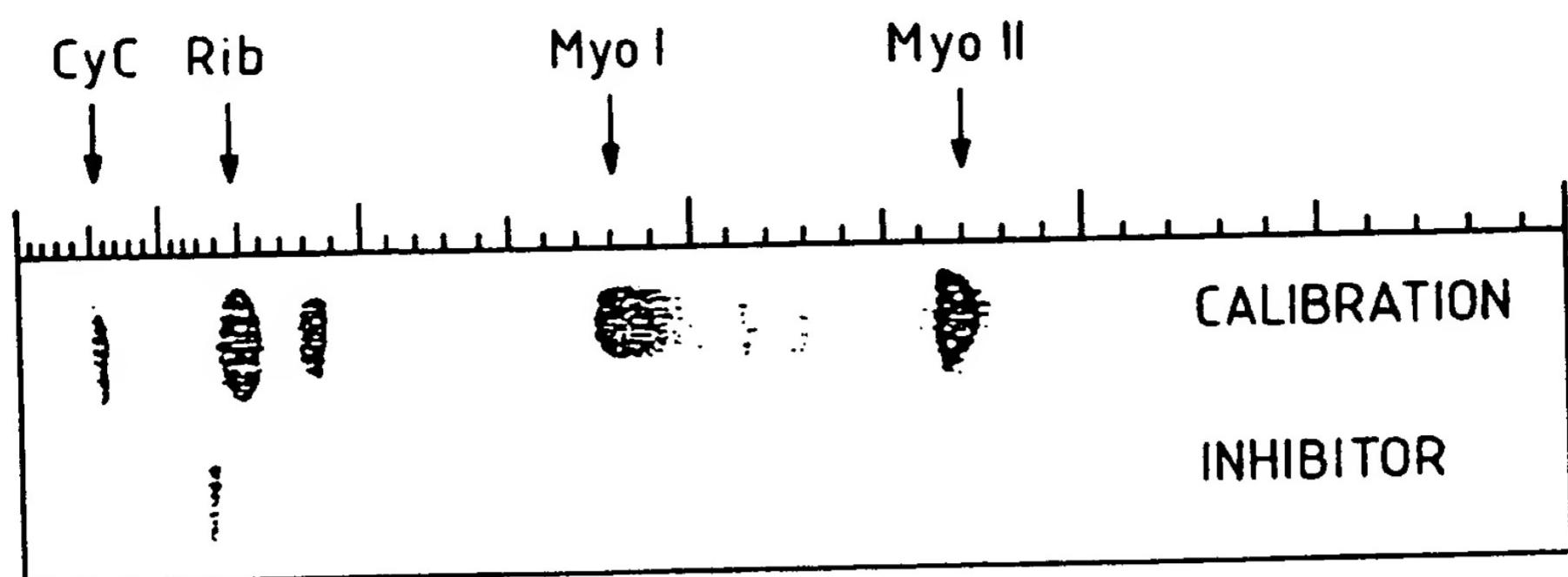


Fig. 8.

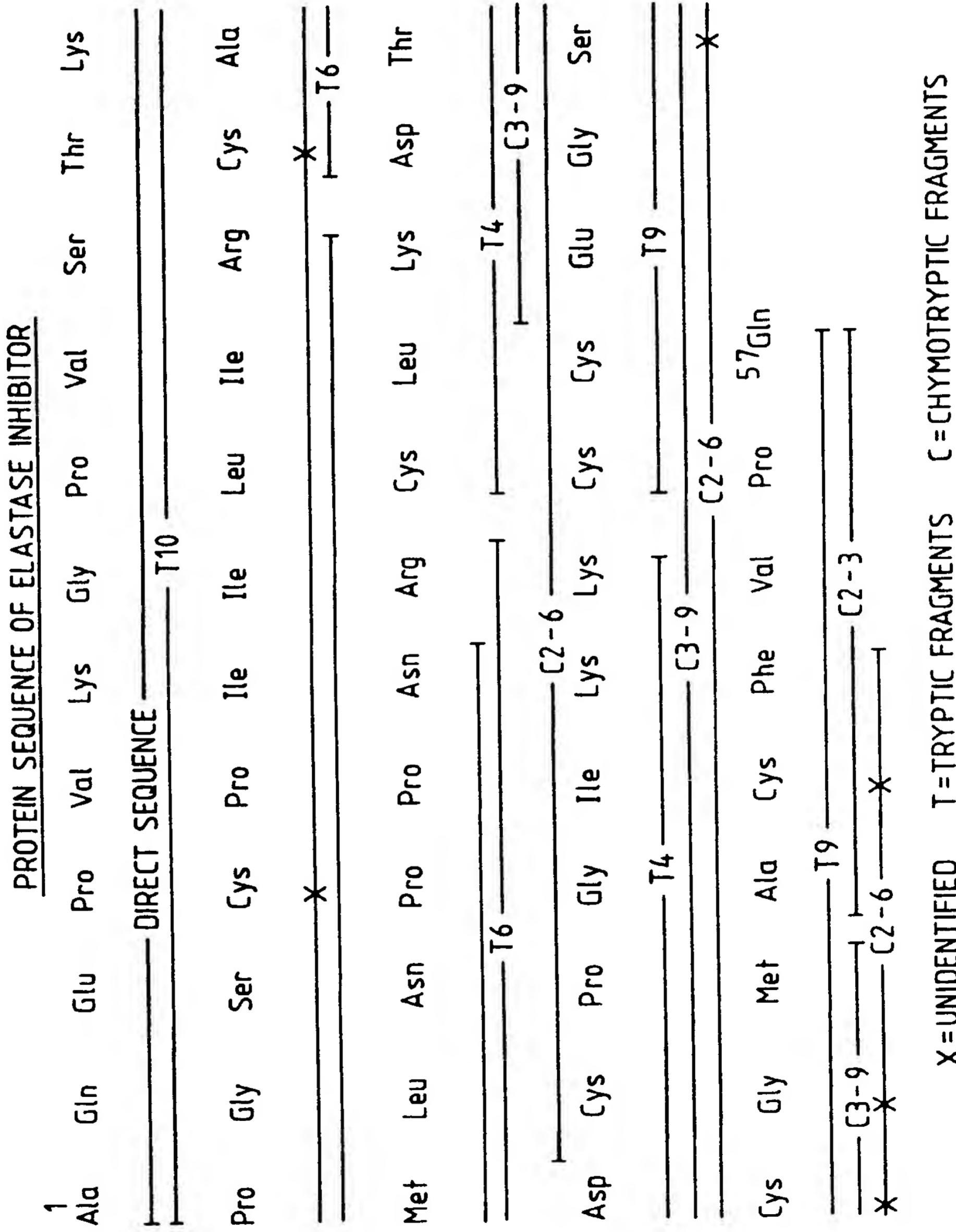


Fig. 9.

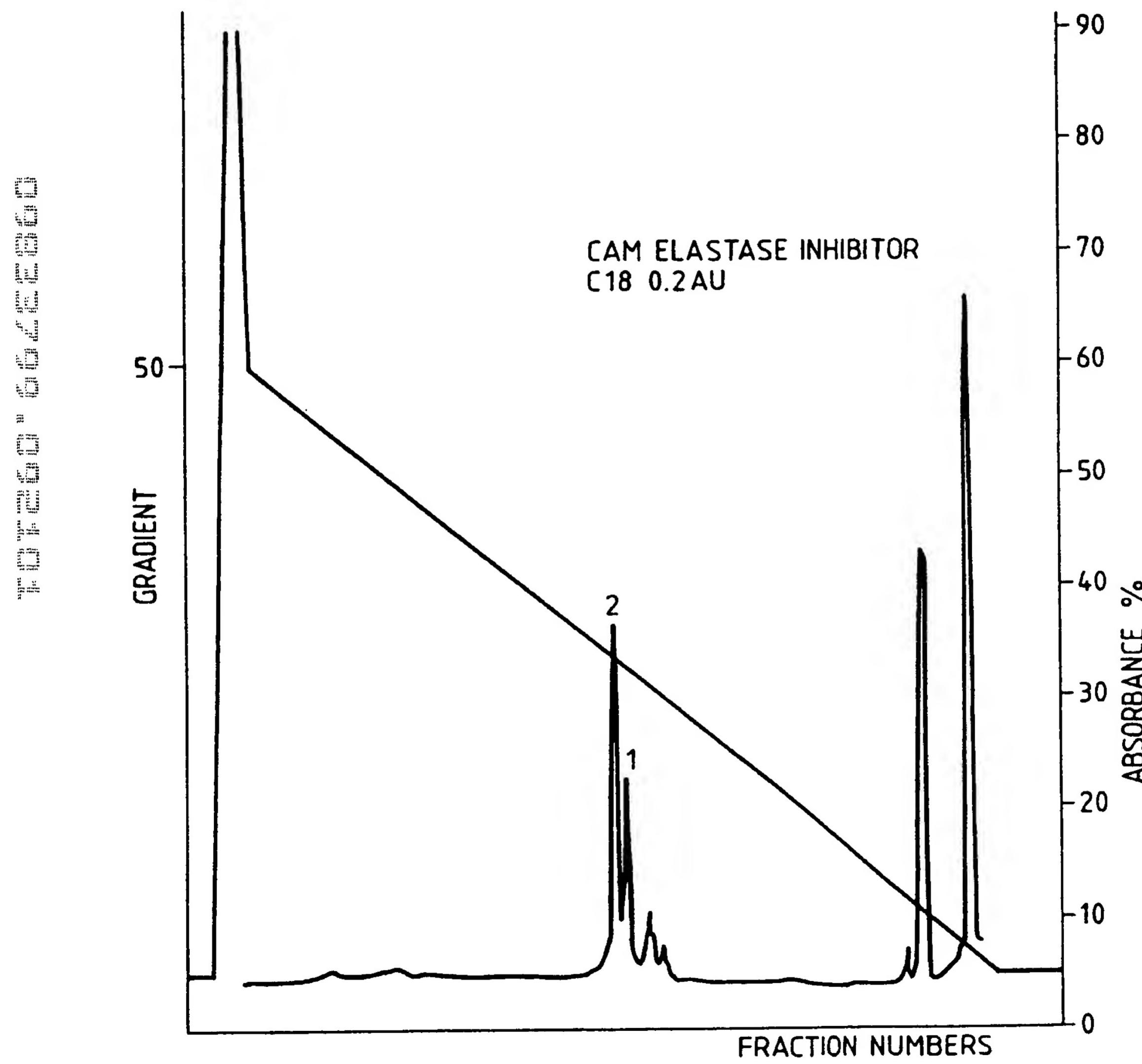


Fig. 10.

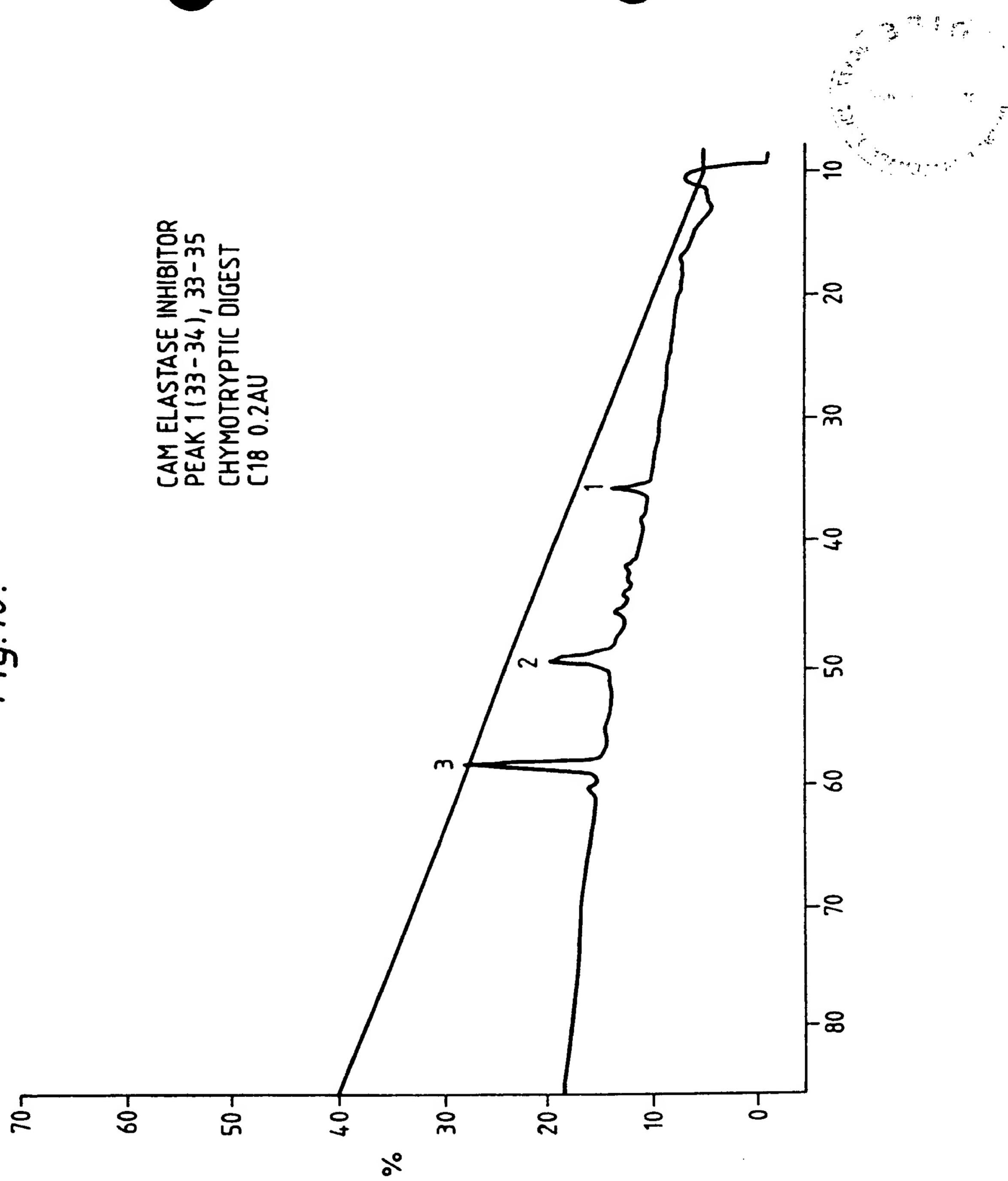


Fig. 11.

100% 90% 80% 70% 60% 50% 40% 30% 20% 10% 0%

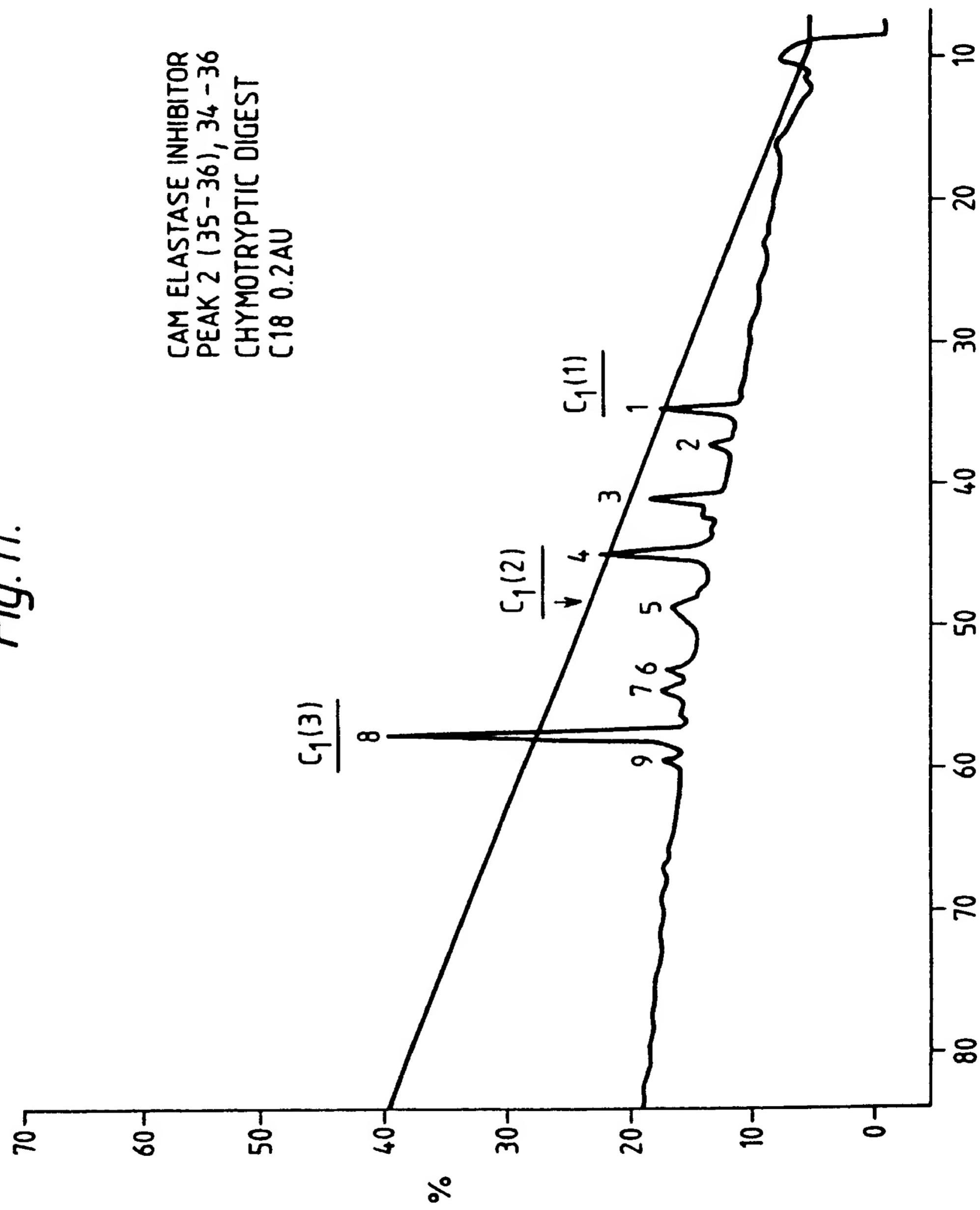


Fig. 12.

100 90 80 70 60 50 40 30 20 10 0

CAM ELASTASE INHIBITOR
(35-36), 34-36
TRYPTIC DIGEST
C18 0.1AU

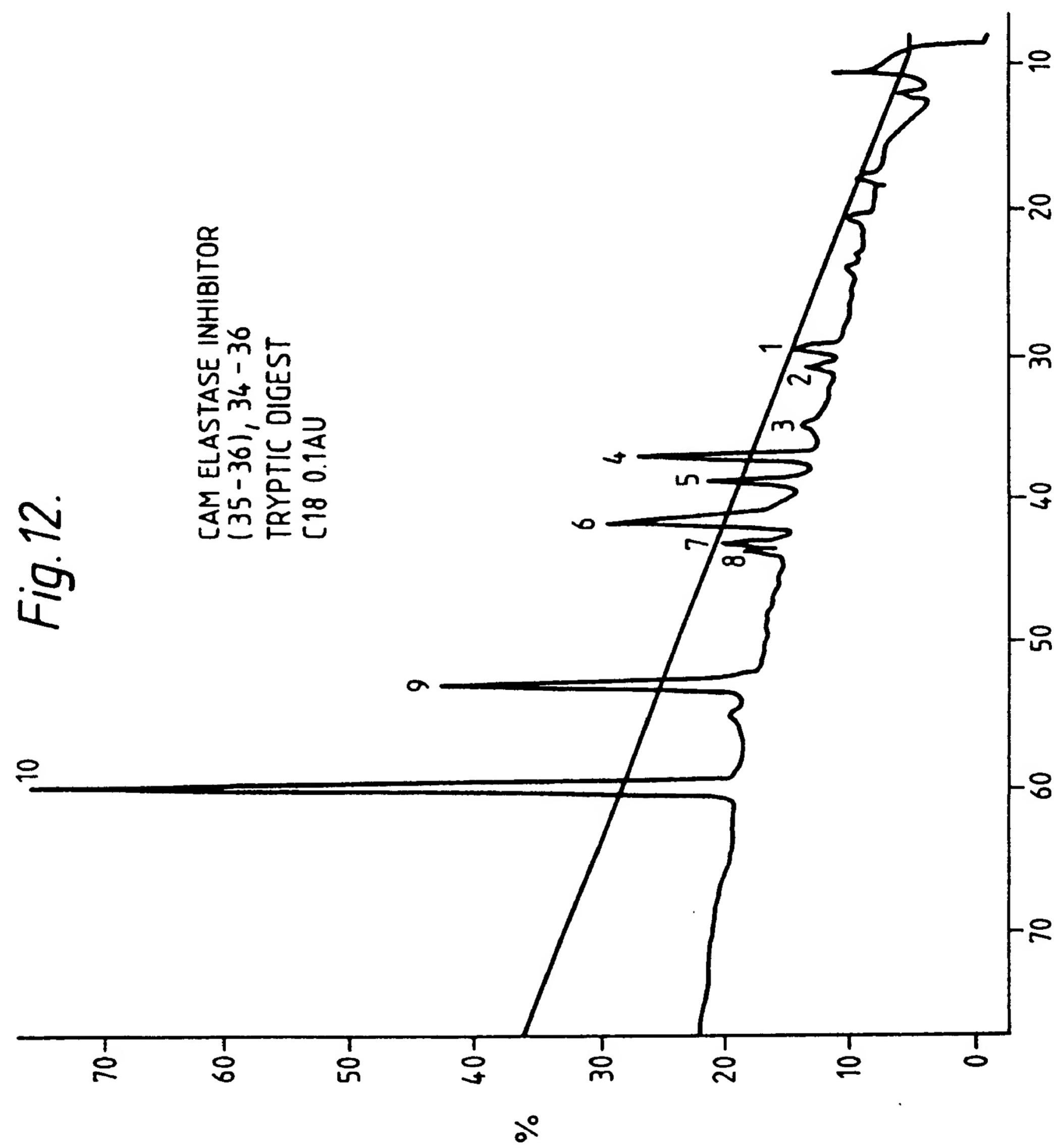


Fig. 13.

AlaGlnGluProValLysGlyProValSerThr

1 ELI1
AATTGAGCTCGTACCATACCTGCATATGCTCAAGAACCAAGTTAAAGGTCTGTCTACT
GCTCGAGCCATGGTATGGACGTATCGAGTTCTGGTCAATTCCAGGACACAGATGA

LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsnArg

63 ELI3
AAGCCAGGTTCTTGTCTTATTATCTTGATTGTTGCGCTATGTTAAACCCACCTAACCGT
TTCGGTCCAAGAACAGGATAATAGAACTAACGAAACCGCGATACAATTGGGTGGATTGGCA
ELI2 ←

CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet

123 ELI5
TGTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGTGAAGGTTCTGCGGTATG
ACAAACTTCTGTGACTAACAGGTCCATAGTTTACGACACTCCAAGGACGCCATAC
ELI4 ←

AlaCysPheValProGlnEndEnd

183 GCTTGTTCGTTCCACAATAATAG

CGAACAAAGCAAGGTGTTATTATCCTAG 210

ELI6 ←

Fig. 14.

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5' DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG

Z = T, C or A

P = A or G

Fig. 19.

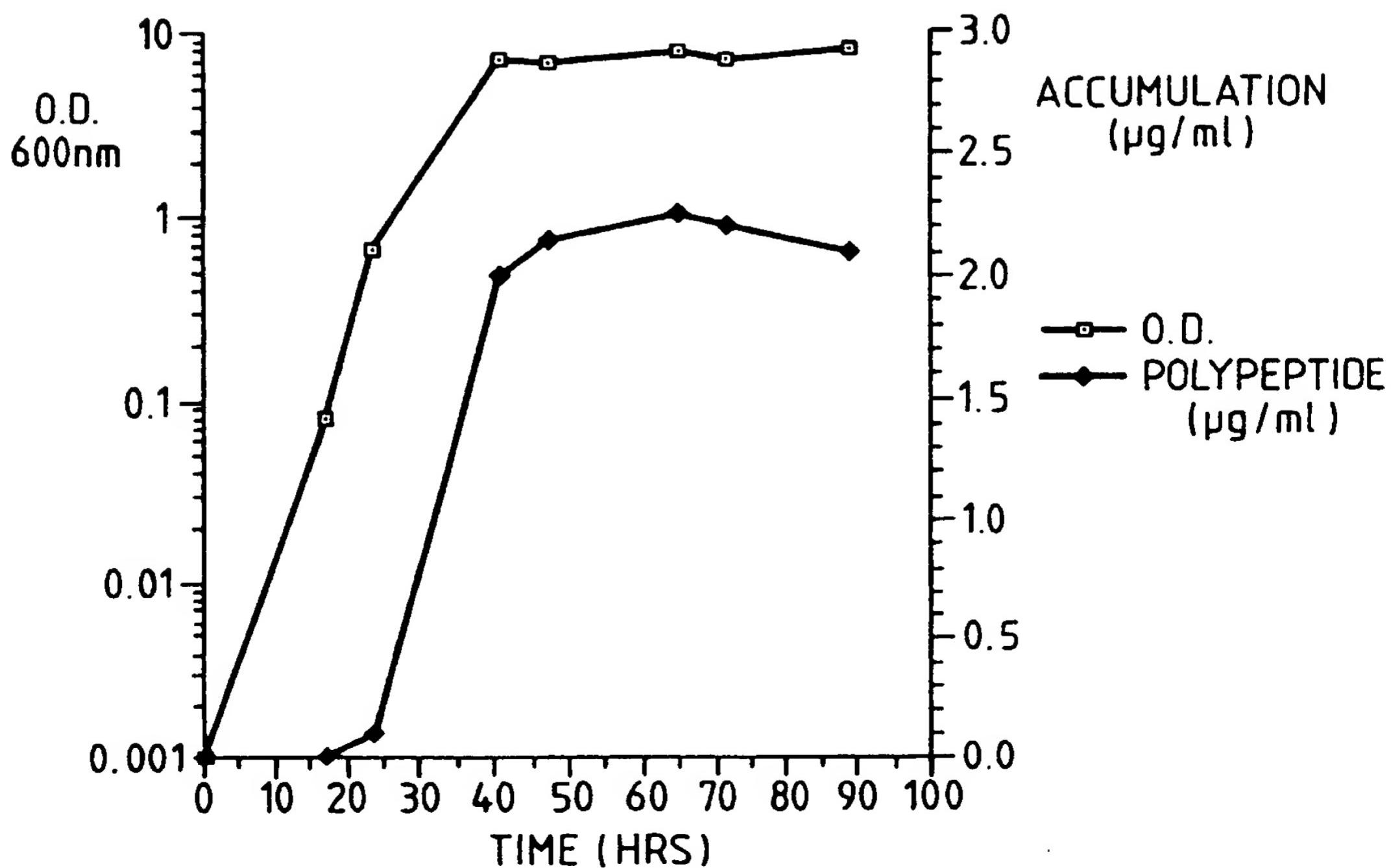


Fig. 15.

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5' DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

GCCGTCCCCAGAGCTACAGGCCCATCTGGTCCTAACGTCCCTGCTGCCCTTCCCTCCACACTGTCCA
TTCTTCCCTCCATTCAAGGATGCCACGGCTGGAGCTGCCTCTCATCCACTTCCAATAAAGAGTTCCG
GAATTC

Poly A 3'
signal

Z = T, C or A

P = A or G

Fig. 16.

Fig. 16 (cont.)

190

210

230

AGTCTCCACTAAGCCTGGCTCCTGCCCATATTATCTTGATCCGGTGC GCCATGTTGAATCC
oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr

250

270

290

CCCTAACCGCTGCTT GAAAGATACTGACTGCCAGGAATCAAGAAGTGCTGTGAAGGCTC
oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe

310

330

350

TTGCGGGATGCCCTGTT CGTCCCCAGTGAGAGGGAGCCGGTCCTGCTGCACCTGTGC
rCysGlyMetAlaCysPheValProGlnEnd

370

390

410

CGTCCCCAGAGCTACAGGCCCATCTGGTCCTAAGTCCCTGCTGCCCTCCCCTCCAC

430

450

470

ACTGTCCATTCTCCTCCCATTAGGATGCCACGGCTGGAGCTGCCTCTCATCCACT

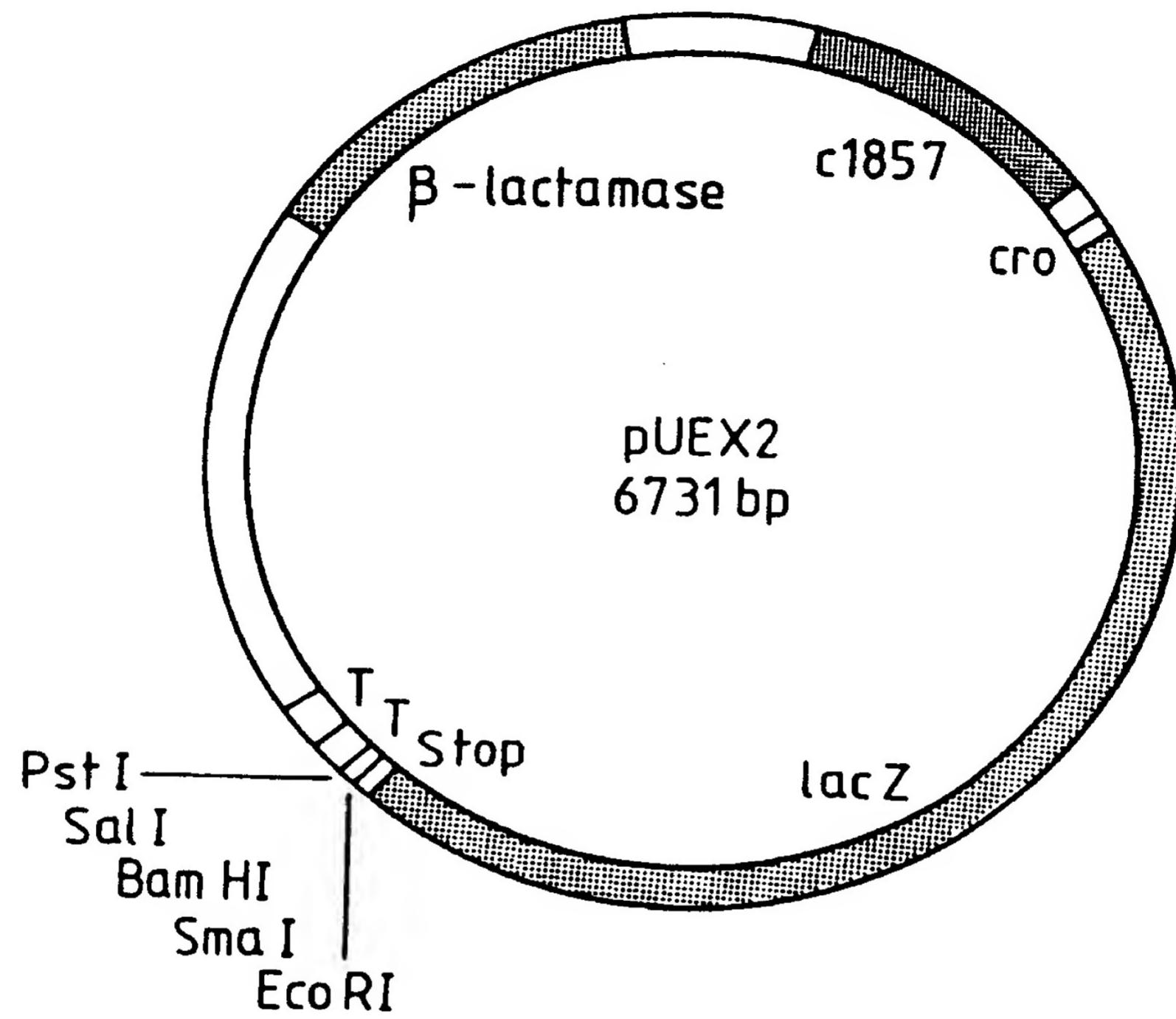
490

TTCCAATAAGAGTTCCCGAATTC

Poly A
signal

EcoRI

Fig. 17.



pUEX2 EcoRI SmaI BamHI SalI PstI
| | | | |
GAA TTC CCG GGG ATC CGT CGA CCT GCA GCC AAG CTT GCT GAT TGA
Glu Phe Pro Gly Ile Arg Arg Pro Ala Ala Lys Leu Ala Asp ***

Fig. 18.

